IN THE SPECIFICATION

Please amend the specification as follows:

Please amend line 18, page 31, as follows:

gene is depicted in SEQ ID ~~NO:9~~ NO:8. A deduced amino acid

Please amend line 20, page 31, as follows:

SEQ ID ~~NO:10~~ NO:9.

Please amend lines 1-6, page 35, as follows:

Be used as the 3′ primer. ~~For example, an oligonucleotide, degenerate or otherwise, that has the degenerate nucleotide sequence YTTYTTNCCNCCNNAGNACNGTNCC (SEQ ID NO:6) or YTTYTTNCCNCCYAANACNGTNCC (SEQ ID NO 8) may be used as the 3′ primter in conjunction with the various 5′ primer discussed above.~~

Please amend line 23, page 53, as follows:

(SEQ ID ~~NO:12~~ NO:11) Additionally, an internal peptide of OMP 106

Please amend line 10, page 56, as follows:

amino acid sequence depicted in SEQ ID ~~NO:12~~ NO:11.

Please amend lines 12-14, page 56, as follows:

24 amino acids (SEQ ID ~~NO:13~~ NO:12) was chosen for the design of the degenerate oligonucleotides MC 11 (SEQ ID ~~NO:14~~ NO:13) and MC 12 (SEQ ID ~~NO:15~~ NO:14), the sequences of which are also shown

Please amend line 17, page 56, as follows:

EADGGKGGANARGDKSIAIGDIAQ (SEQ ID ~~NO:13~~ NO:12)

Please amend lines 19-22, page 56, as follows:

MC 11: GAR GCN GAY GGN GGN AAR (512-fold degenerate) (SEQ ID ~~NO:14~~ NO:13)
MC 12: YTG NGC DAT RTC NCC DAT (576-fold degenerate) (SEQ ID ~~NO:15~~ NO:14).

Please amend line 35, page 56, as follows:

degenerate oligonucleotides MC 11 (SEQ ID ~~NO:14~~ NO:13) and MC 12

Please amend line 1, page 57, with the following

(SEQ ID ~~NO:15~~ NO:14) (0.5 μM each) and 5 U of Taq polymerase using

Please amend lines 1-2, page 58, as follows:

Ser Ile Ala Ile Gly Asp Ile Ala Gln	(SEQ ID ~~NO:19~~ NO:18)
TCC ATT GCT ATT GGT GAC ATT GCG CAA.	(SEQ ~~ID NO:18~~ NO:17)

Please amend line 6, page 58, as follows:

residue 6 of SEQ ID ~~NO:12~~ NO:11.

Please amend line 12, page 58, as follows:

(SEQ ID ~~NO:16~~ NO:15) AND MC 18 (SEQ ID ~~NO:17~~ NO:16), respectively, whose

Please amend lines 15-16, page 58, as follows:

MC 17 : GAA GCG GAC GGG GGG AAA	(SEQ ID ~~NO:16~~ NO:15)
MC 18 : TTG CGC AAT GTC ACC AAT	(SEQ ID ~~NO:17~~ NO: 16)

Place amend line 35, page 59, as follows:

primer pair MC17 (SEQ ~~ID NO:16~~ NO:15) and MC18 (SEQ ID ~~NO:17~~ NO:16) as

Please replace the paragraph beginning at line 32, page 61 through line 2, page 62, with the following:

The kit oligonucleotide P1 (TCATCATTGGAAAACGTTCTTCGGGGCGAA) (SEQ ID NO:19) hybridizes approximately 1 kb away from the multiple cloning site of p *omp* N/P. The size of a PCR product obtained with the oligonucleotides P1 and MC 17 (SEQ ID NO:15) was approximately 1.5 kb. It was hence deduced that the 72 bp fragment maps at approximately 450 bp upstream from the PstI site. It was hence deduced from this information that the major part of the OMP106 protein was encoded by sequences located beyond the PstI site. By the same token, there was ample sequence upstream from the 72 bp region to encode a presumptive signal sequence and promoter/regulator elements to drive transcription of this gene in *Moraxella catarrhalis*.

Please replace the paragraph beginning at line 25, page 63 through line 3, page 64, with the following:

Finally, the missing sequences between the PstI site and the EcoRI were generated by long distance PCR (Barnes, W.M., 1994, Proc. Natl. Acad. Sci. USA 91:2216-2220) using genomic DNA or phageλ *omp*106.6 DNA as the template. The primers for this experiment were MC 17 (SEQ ID NO:15) and a gene-specific primer, *omp* R/X a1 (CGG TCA GCT TAG GCG TGG TT) (SEQ ID NO:20) which was designed based on sequence information downstream from the EcoRI site in pBK *omp* R/X. The PCR product having an approximate size of 3.5 kb was digested with PstI and EcoRI and the approximately 3 kb fragment was gel-isolated and cloned into PstI/EcoRI digested pBluescript II SK. The resulting recombinant plasmid was designated as p *omp* P/R. A map of the *omp*106 locus, including fragments subcloned and used in various constructs, is shown in Figure 11. Construction of the plasmids illustrated in Figure 11 is described herein below in Section 9.

Please amend lines 6-7, page 65, as follows:

is shown in SEQ ~~ID NO:9~~ NO:8. A deduced amino acid sequence of the open reading frame of *omp* 106 is shown in SEQ ID ~~NO:10~~ NO:9.

Please amend lines 2-21, page 85 as follows:

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: ~~24 amino acids~~ 18 base pairs
- (B) TYPE: ~~amino acid~~ nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: ~~peptide~~ other nucleic acid
(A) DESCRIPTION: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

gargcngayg gnggnaar 24

~~Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser~~
~~1 5 10 15~~
~~Ile Ala Ile Gly Asp Ile Ala Gln~~
~~20~~

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 ~~amino acids~~ base pairs
(B) TYPE: ~~amino acid~~ nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: ~~peptide~~ other nucleic acid
(A) DESCRIPTION: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ytgngcdatr tcnccdat 18

~~Gly Ala Arg Gly Cys Asn Gly Ala Tyr Gly Gly Asn Gly Gly Asn Ala~~
~~1 5 10 15~~
~~Ala Arg~~